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RAW SEQUENCE LISTING

DATE: 11/27/2001

PATENT APPLICATION: US/09/856,339A

TIME: 10:15:47

Input Set : A:\Sequence Listing.txt

Output Set : N:\CRF3\11212001\I856339A.raw

ENTERED

11212001\I856339A

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3 <110> APPLICANT: Wong, Luet
4     Bell, Stephen
5     Carmichael, Angus
7 <120> TITLE OF INVENTION: PROCESS FOR OXIDISING TERPENES
9 <130> FILE REFERENCE: HO-P02196US0 (10104571)
11 <140> CURRENT APPLICATION NUMBER: US 09/856,339A
12 <141> CURRENT FILING DATE: 2001-05-18
14 <150> PRIOR APPLICATION NUMBER: PCT/GB99/03873
15 <151> PRIOR FILING DATE: 1999-11-19
17 <150> PRIOR APPLICATION NUMBER: GB 9825421.2
18 <151> PRIOR FILING DATE: 1998-11-19
20 <160> NUMBER OF SEQ ID NOS: 23
22 <170> SOFTWARE: PatentIn version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1242
26 <212> TYPE: DNA
27 <213> ORGANISM: Pseudomonas putida
29 <220> FEATURE:
30 <221> NAME/KEY: misc_feature
31 <222> LOCATION: (1)..(1242)
32 <223> OTHER INFORMATION: Coding sequence
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38 cacctgggat togacttcga catgtacaat cgcgcgaatc tgtctgccgg cgtgcaggag      120
40 gacctgggcag ttctgcaaga atcaaacgta cggatctgg tgtggactcg ctgcaacggc      180
42 ggacactgga tcgccactcg cggccaactg atccgtgagg cctatgaaga ttaccgccac      240
44 ttttcacagcg agtgcccgtt catccctcgt gaagccggcg aagcctacga cttcattccc      300
46 acctcgatgg atccgcccga gcagcgccag tttcgtgcgc tggccaacca agtggttggc      360
48 atgcccgtgg tggataagct ggagaaccgg atccaggagc tggcctgctc gctgatcgag      420
50 agcctgcgcc cgcaaggaca gtgcaacttc accgaggact acgccgaacc cttcccgata      480
52 cgcactttca tgctgctcgc aggtctaccg gaagaagata tcccgcaact gaaataccta      540
54 acggatcaga tgaccgcgtc ggatggcagc atgaccttcg cagaggccaa ggaggcgctc      600
56 tacgactatc tgataccgat catcgagcaa cgcaggcaga agccgggaac cgacgctatc      660
58 agcatcgttg ccaacggcca ggtcaatggg cgaccgatca ccagtgaaga agccaagagg      720
60 atgtgtggcc tgttactggg cggcggcctg gatacgggtg tcaatttctc cagcttcagc      780
62 atggagttcc tggccaaaag cccggagcat cgccaggagc tgatcgagcg tcccagagcg      840
64 attccagccg cttgcgagga actactccgg cgcttctcgc tggttgccga tggccgcac      900
66 ctacactccg attacgagtt tcatggcgtg caactgaaga aaggtgacca gatcctgcta      960
68 ccgcagatgc tgtctggcct ggatgagcgc gaaaacgcct gcccgatgca cgtcgacttc      1020
70 agtcgccaaa aggtttcaca caccaccttt ggccacggca gccatctgtg ccttggccag      1080
72 cacctggccc gccgggaaat catcgtcacc ctcaaggaaat ggctgaccag gattcctgac      1140
74 ttctocattg ccccggtgac ccagattcag cacaagagcg gcatcgctcag cggcgtgcag      1200
76 gcaactccctc tgggtctggga tccggcgact accaaagcgg ta      1242
79 <210> SEQ ID NO: 2
80 <211> LENGTH: 3150
81 <212> TYPE: DNA
82 <213> ORGANISM: Bacillus megaterium
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84 <220> FEATURE:

85 <221> NAME/KEY: misc_feature

86 <222> LOCATION: (1)..(3150)

87 <223> OTHER INFORMATION: Coding sequence

90 <400> SEQUENCE: 2

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95 tttaaattcg aggcgcctgg tcgtgtaacg cgctacttat caagtcagcg tctaattaaa      180
97 gaagcatgcg atgaatcacg ctttgataaa aacttaagtc aagcgcttaa atttgtacgt      240
99 gattttgcag gagacgggtt atttacaagc tggacgcagc aaaaaaattg gaaaaaagcg      300
101 cataatatct tacttccaag cttcagtcag caggcaatga aaggctatca tgcgatgatg      360
103 gtcgatatcg ccgtgcagct tgttcaaaag tgggagcgtc taaatgcaga tgagcatatt      420
105 gaagtaccgg aagacatgac acgtttaacg cttgatacaa ttggtctttg cggctttaac      480
107 tatcgcttta acagctttta ccgagatcag cctcatccat ttattacaag tatggctccg      540
109 gcaactggatg aagcaatgaa caagctgcag cgagcaaatc cagacgaccc agcttatgat      600
111 gaaaacaagc gccagtttca agaagatatc aaggtgatga acgacctagt agataaaaatt      660
113 attgcagatc gcaaagcaag cggatgaaca agcgatgatt tattaacgca tatgctaaac      720
115 ggaaaagatc cagaaacggg tgagccgctt gatgacgaga acattcgcta tcaaattatt      780
117 acattcttaa ttgcgggaca cgaaacaaca agtggctctt tatcatttgc gctgtatttc      840
119 ttagtgaaaa atccacatgt attacaaaaa gcagcagaag aagcagcacg agttctagta      900
121 gatcctgctc caagctacaa acaagtcaaa cagcttaaat atgtcggcat ggtcttaaac      960
123 gaagcgtgct gcttatggcc aactgctcct gcgttttccc tatatgcaa agaagatacg      1020
125 gtgcttgagg gagaatatcc tttagaaaaa ggcgacgaac taatggttct gattcctcag      1080
127 cttcaccgtg ataaaacaat ttggggagac gatgtggaag agttccgtcc agagcgtttt      1140
129 gaaaatccaa gtgcgattcc gcagcatgcg tttaaaccgt ttggaaacgg tcagcgcgcg      1200
131 tgtatcggtc agcagttcgc tcttcatgaa gcaacgctgg tacttggtat gatgctaaaa      1260
133 cactttgact ttgaagatca tacaaactac gagctggata ttaaagaaac tttaacgtta      1320
135 aaacctgaag gctttgtggt aaaagcaaaa tcgaaaaaaa ttccgcttgg cggatttcct      1380
137 tcacctagca ctgaacagtc tgccaaaaaa gcacgcaaaa aggcaaaaa cgctcataat      1440
139 acgcgcgtgc ttgtgctata cggttcaaat atgggaacag ctgaaggaac ggcgcgtgat      1500
141 ttagcagata ttgcaatgag caaaggattt gcaccgcagg tcgcaacgct tgattcacac      1560
143 gccggaaatc ttccgcgcga aggagctgta ttaattgtaa cggcgtctta taacggtcat      1620
145 ccgcctgata acgcaagca atttgcgac tgggttagacc aagcgtctgc tgatgaagta      1680
147 aaaggcgctt gctactccgt atttggatgc ggcgataaaa actgggctac tacgtatcaa      1740
149 aaagtgcctg cttttatcga tgaaacgctt gccgctaaag gggcagaaaa catcgctgac      1800
151 cgcggtgaag cagatgcaag cgacgacttt gaaggcacat atgaagaatg gcgtgaacat      1860
153 atgtggagtg acgtagcagc ctactttaac ctgcacattg aaaacagtga agataataaa      1920
155 tctactcttt cacttcaatt tgtcgacagc gccgcggata tgccgcttgc gaaaatgcac      1980
157 ggtgcgtttt caacgaacgt cgtagcaagc aaagaacttc aacagccagg cagtgcacga      2040
159 agcacgcgac atcttgaaat tgaacttcca aaagaagctt cttatcaaga aggagatcat      2100
161 ttaggtgtta ttctcgcgaa ctatgaagga atagtaaacc gtgtaacagc aaggttcggc      2160
163 ctatgatgat cacagcaaat ccgtctggaa gcagaagaag aaaaattagc tcatttgcca      2220
165 ctgcgtaaaa cagtatccgt agaagagctt ctgcaatacg tggagcttca agatcctggt      2280
167 acgcgcacgc agcttcgcgc aatggctgct aaaacggctc gcccgccgca taaagtagag      2340
169 cttgaagcct tgcttgaaaa gcaagcctac aaagaacaag tgctggcaaa acgtttaaca      2400
171 atgcttgaaac tgcttgaaaa ataccggcg tgtgaaatga aattcagcga atttatcgcc      2460
173 cttctgccaa gcatacgccc gcgctattac tcgatttctt catcacctcg tgcgatgaa      2520
175 aaacaagcaa gcatcacggt cagcgttgtc tcaggagaag cgtggagcgg atatggagaa      2580
177 tataaaggaa ttgcgtcgaa ctatcttgcc gagctgcaag aaggagatac gattacgtgc      2640

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179 tttattttcca caccgcagtc agaatttacg ctgccaaaag accctgaaac gccgcttata 2700
181 atggtcggac cgggaacagg cgtcgcgccg tttagaggct ttgtgcaggc gcgcaaacag 2760
183 ctaaaagaac aaggacagtc acttgagaga gcacatttat acttcggctg ccgttcacct 2820
185 catgaagact atctgtatca agaagagctt gaaaacgccc aaagcgaagg catcattacg 2880
187 cttcataccg ctttttctcg catgccaaat cagccgaaaa catacgttca gcacgtaatg 2940
189 gaacaagacg gcaagaaatt gattgaactt cttgatcaag gagcgcactt ctatatttgc 3000
191 ggagacggaa gccaaatggc acctgccgtt gaagcaacgc ttatgaaaag ctatgctgac 3060
193 gttcaccaag tgagtgaagc agacgctcgc ttatggctgc agcagctaga agaaaaaggc 3120
195 cgatacgcaa aagacgtgtg ggctgggtaa 3150
198 <210> SEQ ID NO: 3
199 <211> LENGTH: 7
200 <212> TYPE: PRT
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <221> NAME/KEY: DOMAIN
205 <222> LOCATION: (1)..(7)
206 <223> OTHER INFORMATION: Synthetic linker
209 <400> SEQUENCE: 3
211 Thr Asp Gly Thr Ser Ser Thr
212 1 5
214 <210> SEQ ID NO: 4
215 <211> LENGTH: 7
216 <212> TYPE: PRT
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <221> NAME/KEY: DOMAIN
221 <222> LOCATION: (1)..(7)
222 <223> OTHER INFORMATION: Synthetic Linker
225 <400> SEQUENCE: 4
227 Thr Asp Gly Ala Ser Ser Ser
228 1 5
230 <210> SEQ ID NO: 5
231 <211> LENGTH: 17
232 <212> TYPE: PRT
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <221> NAME/KEY: DOMAIN
237 <222> LOCATION: (1)..(17)
238 <223> OTHER INFORMATION: Synthetic Linker
241 <400> SEQUENCE: 5
243 Thr Asp Gly Thr Arg Pro Gly Pro Gly Pro Gly Pro Gly Pro Ser Ser
244 1 5 10 15
246 Thr
249 <210> SEQ ID NO: 6
250 <211> LENGTH: 21
251 <212> TYPE: PRT
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <221> NAME/KEY: DOMAIN

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256 <222> LOCATION: (1)..(21)
257 <223> OTHER INFORMATION: Synthetic Linker
260 <400> SEQUENCE: 6
262 Thr Asp Gly Thr Arg Pro Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro
263 1 5 10 15
265 Gly Pro Ser Ser Thr
266 20
268 <210> SEQ ID NO: 7
269 <211> LENGTH: 4
270 <212> TYPE: PRT
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <221> NAME/KEY: DOMAIN
275 <222> LOCATION: (1)..(4)
276 <223> OTHER INFORMATION: Synthetic Linker
279 <400> SEQUENCE: 7
281 Pro Leu Glu Leu
282 1
284 <210> SEQ ID NO: 8
285 <211> LENGTH: 7
286 <212> TYPE: PRT
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <221> NAME/KEY: DOMAIN
291 <222> LOCATION: (1)..(7)
292 <223> OTHER INFORMATION: Synthetic Linker
295 <400> SEQUENCE: 8
297 Thr Asp Gly Gly Ser Ser Ser
298 1 5
300 <210> SEQ ID NO: 9
301 <211> LENGTH: 51
302 <212> TYPE: DNA
303 <213> ORGANISM: Artificial Sequence
305 <220> FEATURE:
306 <221> NAME/KEY: misc_feature
307 <222> LOCATION: (1)..(51)
308 <223> OTHER INFORMATION: Synthetic Primer
311 <400> SEQUENCE: 9
312 gagattaaga attcataaac acatgggagt gcgtgccata tgaacgcaaa c 51
315 <210> SEQ ID NO: 10
316 <211> LENGTH: 36
317 <212> TYPE: DNA
318 <213> ORGANISM: Artificial Sequence
320 <220> FEATURE:
321 <221> NAME/KEY: variation
322 <222> LOCATION: (1)..(36)
323 <223> OTHER INFORMATION: Synthetic desired coding sequence
326 <400> SEQUENCE: 10
327 gaactgagta gtgccactga cggaggatcc tcatcg 36

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330 <210> SEQ ID NO: 11
331 <211> LENGTH: 36
332 <212> TYPE: DNA
333 <213> ORGANISM: Artificial Sequence
335 <220> FEATURE:
336 <221> NAME/KEY: misc_feature
337 <222> LOCATION: (1)..(36)
338 <223> OTHER INFORMATION: Synthetic Primer
341 <400> SEQUENCE: 11
342 cgatgaggat cctccgtcag tggcactact cagttc          36
345 <210> SEQ ID NO: 12
346 <211> LENGTH: 36
347 <212> TYPE: DNA
348 <213> ORGANISM: ARTIFICIAL SEQUENCE
350 <220> FEATURE:
351 <221> NAME/KEY: misc_feature
352 <222> LOCATION: (1)..(36)
353 <223> OTHER INFORMATION: Synthetic Primer
356 <400> SEQUENCE: 12
357 tcatcgggat cctcatcgat gtctaaagta gtgtat          36
360 <210> SEQ ID NO: 13
361 <211> LENGTH: 52
362 <212> TYPE: DNA
363 <213> ORGANISM: Artificial Sequence
365 <220> FEATURE:
366 <221> NAME/KEY: misc_feature
367 <222> LOCATION: (1)..(52)
368 <223> OTHER INFORMATION: Synthetic desired coding sequence
371 <400> SEQUENCE: 13
372 cccgataggc aatggtaatc atcgggagtc tagagcatcg aagctttcat cg          52
375 <210> SEQ ID NO: 14
376 <211> LENGTH: 52
377 <212> TYPE: DNA
378 <213> ORGANISM: Artificial Sequence
380 <220> FEATURE:
381 <221> NAME/KEY: misc_feature
382 <222> LOCATION: (1)..(52)
383 <223> OTHER INFORMATION: Synthetic Primer
386 <400> SEQUENCE: 14
387 cgatgaaagc ttgatgctc tagactcccg atgattacca ttgcctatcg gg          52
390 <210> SEQ ID NO: 15
391 <211> LENGTH: 24
392 <212> TYPE: DNA
393 <213> ORGANISM: Artificial Sequence
395 <220> FEATURE:
396 <221> NAME/KEY: misc_feature
397 <222> LOCATION: (1)..(24)
398 <223> OTHER INFORMATION: Synthetic Primer
401 <400> SEQUENCE: 15

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VERIFICATION SUMMARY

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